

Fig. 1A

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E	G	W	S	S	L	L	R	T	V	H	S	V	L	N	R	S	P	P	E	175
GAG	GGC	TGG	TCC	TCC	CTC	CTC	CGC	ACC	GTC	CAC	AGT	GTG	CTC	AAT	CGC	TCG	CCT	CCA	GAG	525
L	V	A	E	I	V	L	V	D	D	F	S	D	R	E	H	L	K	K	P	195
CTG	GTC	GCC	GAG	ATT	GTA	CTG	GTC	GAC	GAC	TTC	AGT	GAT	CGA	GAG	CAC	CTG	AAG	AAG	CCT	585
L	E	D	Y	M	A	L	F	P	S	V	R	I	L	R	T	K	K	R	E	215
CTT	GAA	GAC	TAC	ATG	GCC	CTT	TTC	CCC	AGT	GTG	AGG	ATT	CTT	CGA	ACC	AAG	AAA	CGG	GAA	645
G	L	I	R	T	R	M	L	G	A	S	V	A	T	G	D	V	I	T	F	235
GGG	CTG	ATA	AGG	ACC	CGA	ATG	CTG	GGG	GCC	TCA	GTG	GCA	ACT	GGG	GAT	GTC	ATC	ACA	TTC	705
L	D	S	H	C	E	A	N	V	N	W	L	P	P	L	L	D	R	I	A	255
TTG	GAT	TCA	CAC	TGT	GAA	GCC	AAT	GTC	AAC	TGG	CTT	CCC	CCC	TTG	CTT	GAC	CGC	ATT	GCT	765
R	N	R	K	T	I	V	C	P	M	I	D	V	I	D	H	D	D	F	R	275
CGG	AAC	CGC	AAG	ACC	ATT	GTG	TGC	CCG	ATG	ATT	GAT	GTA	ATT	GAC	CAT	GAC	GAC	TTT	CGG	825
Y	E	T	Q	A	G	D	A	M	R	G	A	F	D	W	E	M	Y	Y	K	295
TAC	GAG	ACA	CAG	GCA	GGG	GAT	GCC	ATG	CGG	GGA	GCC	TTT	GAC	TGG	GAG	ATG	TAC	TAC	AAG	885
R	I	P	I	P	P	E	L	Q	K	A	D	P	S	D	P	F	E	S	P	315
CGG	ATC	CCG	ATC	CCT	CCA	GAA	CTG	CAG	AAA	GCT	GAC	CCC	AGC	GAC	CCA	TTT	GAG	TCT	CCC	945
V	M	A	G	G	L	F	A	V	D	R	K	W	F	W	E	L	G	G	Y	335
GTG	ATG	GCC	GGT	GGA	CTG	TTC	GCC	GTG	GAT	CGG	AAG	TGG	TTC	TGG	GAA	CTC	GGC	GGG	TAT	1005

Fig. 1B

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D	P	G	L	E	I	W	G	G	E	Q	Y	E	I	S	F	K	V	W	M	355
GAC	CCA	GGC	TTG	GAG	ATC	TGG	GGA	GGG	GAG	CAG	TAT	GAA	ATC	TCC	TTC	AAG	GTG	TGG	ATG	1065
C	G	G	R	M	E	D	I	P	C	S	R	V	G	H	I	Y	R	K	Y	375
TGT	GGG	GGC	CGC	ATG	GAG	GAC	ATC	CCC	TGC	TCC	AGG	GTG	GGC	CAT	ATC	TAC	AGG	AAG	TAT	1125
V	P	Y	K	V	P	A	G	V	S	L	A	R	N	L	K	R	V	A	E	395
GTG	CCC	TAC	AAG	GTC	CCG	GCC	GGA	GTC	AGC	CTG	GCC	CGG	AAC	CTT	AAG	CGG	GTG	GCC	GAA	1185
V	W	M	D	E	Y	A	E	Y	I	Y	Q	R	R	P	E	Y	R	H	L	415
GTG	TGG	ATG	GAT	GAG	TAC	GCA	GAG	TAC	ATT	TAC	CAG	CGC	CGG	CCT	GAA	TAC	CGC	CAC	CTC	1245
S	A	G	D	V	A	V	Q	K	K	L	R	S	S	L	N	C	K	S	F	435
TCC	GCT	GGG	GAT	GTC	GCA	GTC	CAG	AAA	AAG	CTC	CGC	AGC	TCC	CTT	AAC	TGC	AAG	AGT	TTC	1305
K	W	F	M	T	K	I	A	W	D	L	P	K	F	Y	P	P	V	E	P	455
AAG	TGG	TTT	ATG	ACG	AAG	ATA	GCC	TGG	GAC	CTG	CCC	AAA	TTC	TAC	CCA	CCC	GTG	GAG	CCC	1365
P	A	A	A	W	G	E	I	R	N	V	G	T	G	L	C	A	D	T	K	475
CCG	GCT	GCA	GCT	TGG	GGG	GAG	ATC	CGA	AAT	GTG	GGC	ACA	GGG	CTG	TGT	GCA	GAC	ACA	AAG	1425
H	G	A	L	G	S	P	L	R	L	E	G	C	V	R	G	R	G	E	A	495
CAC	GGG	GCC	TTG	GGC	TCC	CCA	CTA	AGG	CTA	GAG	GGC	TGC	GTC	CGA	GGC	CGT	GGG	GAG	GCT	1485
A	W	N	N	M	Q	V	F	T	F	T	W	R	E	D	I	R	P	G	D	515
GCC	TGG	AAC	AAC	ATG	CAG	GTA	TTC	ACC	TTC	ACC	TGG	AGA	GAG	GAC	ATC	CGG	CCT	GGA	GAC	1545

Fig. 1C

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P Q H T K K F C F D A I S H T S P V T L 535
CCC CAG CAC ACC AAG AAG TTC TGC TTT GAT GCC ATT TCC CAC ACC AGC CCT GTC ACG CTG 1605

Y D C H S M K G N Q L W K Y R K D K T L 555
TAC GAC TGC CAC AGC ATG AAG GGC AAC CAG CAG CTG TGG AAA TAC CGC AAA GAC AAG ACC CTG 1665

Y H P V S G S C M D C S E S D H R I F M 575
TAC CAC CCT GTC AGT GGC AGC TGC ATG GAC TGC AGT GAA AGT GAC CAT AGG ATC TTC ATG 1725

N T C N P S S L T Q Q CAG CAG TGG CTG TTT GAA CAC ACC AAC TCA ACA 1785
AAC ACC TGC AAC CCA TCC TCT CTC ACC CAG CAG TGG CTG TTT GAA CAC ACC AAC TCA ACA 1785

V L E K F N R N * 603
GTC TTG GAA AAA TTC AAT AGG AAC TGA 1812

GCCCTCATGTCCCTTGGCAGGCCCCCGGGTCTGGCACTCACTGCAGACTTCCTCTTTCAAGGGAGGCAGGGCCCCCT
GTGGGCACTAGGTGTAAAGGTGCTGGCCAAATGGTTGAGGTGAAGAGGGCTCTTGATTCAAGGGGCTGGGGTCTGCCCT
GGTCCCTGAGCCCCCTGAGTTGTGGGGGTAGGGTGAAGAGCATATCCCAAGAGAGGCCCCACAGGGAGCAGAGACTGCTT
TAATCCCTGCTGACATCACGGAAGCAACAGAGCCCTTTTCAACTTTGTCACTATGTCCCCCTGAGATGGCTCTCCTACATGATGG
AACACCAAGGTAGCCTAGGCCACCCAAAGTAGTCTCGGAGGTGCCCAGCCCTCAGATGGCTCTCCTACATGATGG
TGCTTTAGAAACAAGGTAAATTTGCCCTGTTTGGGGCAGCTTTTAGTATCGATGCCACTCATCTGCAGCAGAAAGAGAA
AGAACTCCTCTTGGGGCTTTTAGTTTCTGCCGTCTGGGGGAACATTGCAGTTACTGCACAGCTTCTGTTCTCTGTC
ACAACCCAGGTGATTTGGTCCGGTCAAAAGGCCATACCTTGGGGCCCTAAGAGTGTTCAGTATTGAATGCTGATCAGCTG
CCAGGTAGGAGTCAGAAAGAGGAGCCCCCTAGACATTTCTTTGCAGCTATGGACATCGGGGATATCTCCCCCTGCTC
TCTGGGTATTTGAAATGTCAATTTTAGCACTCTCCAGGCACAAGGACAGCCACAGCTTTACAGGGCAGTGTTC

Fig. 1D

AGATGGCCCTGAGCCACGGAAAAGGCCAGGTAGACCTCCAAACTAGAAAATGCTGGCTGATTTGCCCCTGATCCCATGCTT
CCATTTCCCTGTCTCTCTCCCCAGGCAATTACTGGCTCAAAAGAGGAACAGAGGTGCTGCGAGGTGCTCACCTCACAC
GAGTCTGGAGGCCCTCCAGGATCAACTGTGGGCAAAAGTGCCTGCCCTCTGACCTCATCATGGTTCTAGTTCTCATACAGAA
CTCCAGAATTTTAAAGAACTCTATAATTGGATTGCAAACTAGGATGCTACATAGGATTCTGGTATTCCACATCCCAATA
TGGATTTCTAGAAATGCTGTGATTAAAGGAGCCAGCCAGGTGTAATACAGTCAAGCAGCCCCCAGCCTAGAGACAATCT
GTGAAATCCAAAGTTGGTGTGGGAAAGCAGGGGACATGTGTCCCTCAGCTCAGCAGAGGCTGTGGTACAAACATG
GTCCTTGGTGAAGACCTGCACCCCTGGAACCTCCCAACCATCATCACTGAGTCTCATTTGCAAGTGGAGAAAAGAAC
CCGACGTCCACAGCCAGATATACCCAGCTCCATGCCAGCCCTTCATGTTTACCTTTTGTGTTAAATTACATGTC
AGACTCCTAGAGGGCTCCAGACTAATAGGAAGCATTTCTGTAAACCAACCTGCCACCCACTGATTCAGAAAATGGAAATC
ACATTCACAAATCTATGGCTTCACCCAGCTAGCCCAGGAAATACTTGAAATCAGCATTCCTCAATAGTGTGAGTCTCTT
GATTGTGTCATTACCAATTAAATAAATGAGACCTAAGTCTGGGAACAGAGCCACGAAATCTGCCCTTTGAGATGCTGGCA
GATCTCAAGGCCATCAATTAATGGGGAGGGAGGACAAACACTCCCAATCATCCACCACTCAGACTGAATGTGTAGCT
GGCGAGGAATTACTTCCACTTCTGGCCCCAGCACAAAGCCCTGCTTTGGCCACCTGTCTGCAAGAGAGGGCCCCCTGTGC
TTGCAACGCTTACGTGTTGATCCAGTGTCCCTTTTCCAAATGAGTGTGTAGCTTTAGAAAGTGGCCCCCTCTATAGAAAAG
AGTCAAAAGATGAGGCCCTTCTAGAAATCTAGGATAACAAGAGTGTGACAGTTTGAGGAGTCCGAATTGAGATTCATCA
TCAAAAGAGCAATGCAGCGTCGTTAAAATAAAAACTGTGCCTTTTAAAAAGAAAAATGCAAAATATAGAGCAAAATCCCTAA
ACTTGAAAAAATAAAAAA

Fig. 1E

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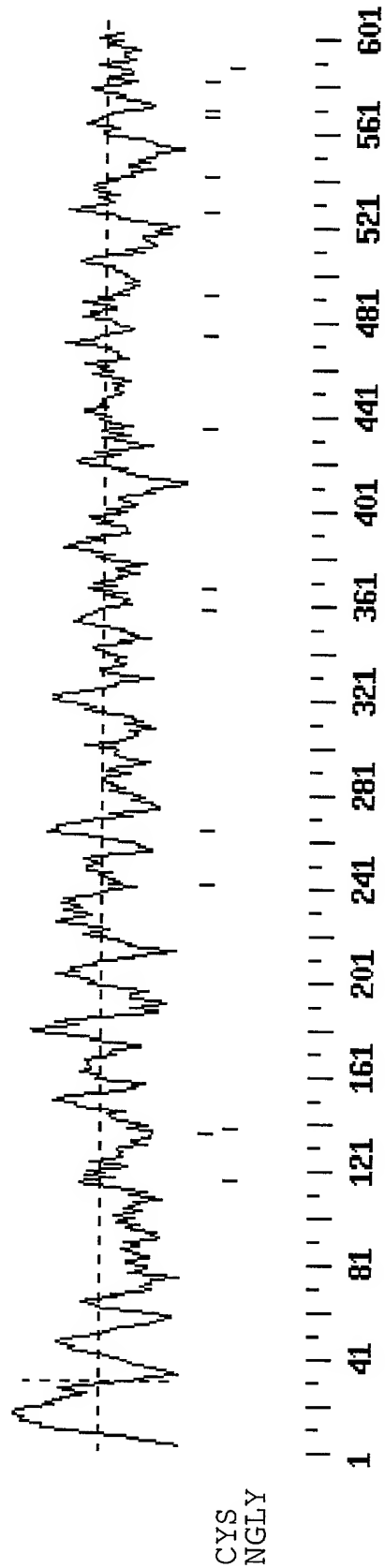


Fig. 2

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M	A	A	G	E	R	S	W	C	L	C	K	L	L	R	F	F	17
TCGGCGGAAG	ATG	GCG	GCC	GCG	GAA	AGG	AGC	TGG	TGC	CTG	TGC	AAG	TTG	TTG	AGG	TTT	51
Y	S	L	F	P	G	L	I	V	C	G	T	L	C	V	C	L	37
TAT	TCA	TTA	TTC	TTC	CCT	GGG	CTC	ATT	GTA	TGT	GGA	ACT	TTA	TGT	GTG	TGT	111
V	L	W	G	I	R	L	L	L	Q	R	K	K	L	V	S	T	57
GTC	CTT	TGG	GGA	ATC	AGA	CTG	CTG	CTA	CAG	AGA	AAG	AAA	TTA	GTG	TCA	ACT	171
N	G	K	N	Q	M	V	I	A	F	H	P	Y	C	N	A	G	77
AAT	GGG	AAA	AAT	CAA	ATG	GTG	ATT	GCA	TTT	TTT	CAT	CCA	TAC	TGC	AAT	GCT	231
G	E	R	V	L	W	C	A	L	R	A	L	Q	K	K	Y	P	97
GGA	GAA	AGA	GTT	TTA	TGG	TGT	GCT	TTA	AGA	GCC	CTG	CAG	AAA	AAG	TAT	CCT	291
Y	V	V	Y	T	G	D	V	N	V	N	G	Q	Q	I	L	E	117
TAT	GTT	GTT	TAT	ACC	GGC	GAT	GTT	AAT	GTC	AAC	GGT	CAA	CAG	ATA	CTA	GAA	351
R	R	F	N	I	R	L	I	H	P	V	Q	F	V	F	L	R	137
AGA	AGA	TTT	AAC	ATC	AGA	TTA	ATT	CAC	CCA	GTG	CAG	TTT	GTT	TTT	TTA	AGG	411
L	V	E	D	S	L	Y	P	H	F	T	L	L	G	Q	S	L	157
CTT	GTG	GAA	GAT	TCA	CTG	TAT	CCT	CAC	TTC	ACA	CTG	CTG	GGC	CAA	AGT	CTA	471
F	L	G	W	E	A	L	M	Q	C	V	P	D	V	Y	I	D	177
TTT	CTT	GGC	TGG	GAA	GCT	CTA	ATG	CAG	TGT	GTT	CCT	GAT	GTT	TAC	ATT	GAT	531

Fig. 3A

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Y	A	F	T	L	P	L	F	K	Y	I	G	G	C	Q	V	G	S	Y	V	197
TAC	GCT	TTT	ACG	CTT	CCT	CTG	TTT	AAG	TAT	ATA	GGG	GGT	TGC	CAA	GTT	GGA	AGC	TAT	GTT	591
H	Y	P	T	I	S	T	D	M	L	S	V	V	K	N	Q	N	I	G	F	217
CAT	TAT	CCT	ACT	ATC	AGC	ACC	GAC	ATG	CTC	TCT	GTA	GTG	AAG	AAT	CAA	AAT	ATT	GGA	TTT	651
N	N	A	A	F	I	T	R	N	P	F	L	S	K	V	K	L	I	Y	Y	237
AAT	AAT	GCA	GCC	TTC	ATT	ACC	AGG	AAT	CCT	TTT	CTC	AGC	AAA	GTA	AAG	CTC	ATC	TAC	TAC	711
Y	L	F	A	F	I	Y	G	L	V	G	S	C	S	D	V	V	M	V	N	257
TAT	TTA	TTT	GCT	TTT	ATT	TAT	GGA	CTT	GTT	GGT	TCT	TGC	AGT	GAT	GTA	GTC	ATG	GTC	AAT	771
S	S	W	T	L	N	H	I	L	S	L	W	K	V	G	N	C	T	N	I	277
TCT	TCT	TGG	ACA	CTA	AAC	CAT	ATT	CTC	TCA	CTA	TGG	AAA	GTT	GGG	AAT	TGC	ACT	AAC	ATT	831
V	Y	P	P	C	D	V	Q	T	F	L	D	I	P	L	H	E	K	K	M	297
GTT	TAT	CCA	CCT	TGT	GAT	GTG	CAG	ACA	TTT	CTG	GAC	ATT	CCC	TTA	CAT	GAG	AAA	AAG	ATG	891
T	P	G	H	L	L	V	S	V	G	Q	F	R	P	E	K	N	H	P	L	317
ACC	CCA	GGA	CAT	TTG	CTG	GTT	TCT	GTT	GGC	CAG	TTT	AGG	CCG	GAA	AAG	AAT	CAT	CCA	TTG	951
Q	I	R	A	F	A	K	L	L	N	K	K	M	V	E	S	P	P	S	L	337
CAG	ATC	AGA	GCC	TTT	GCT	AAA	TTG	CTG	AAT	AAG	ATG	GTT	GAG	TCA	CCT	CCT	TCG	CTT	1011	
K	L	V	L	I	G	G	C	R	N	K	D	D	E	L	R	V	N	Q	L	357
AAA	CTT	GTC	CTC	ATT	GGA	GGT	TGT	CGT	AAC	AAA	GAT	GAT	GAA	CTT	AGG	GTA	AAC	CAA	CTG	1071

Fig. 3B

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R	R	L	S	E	D	L	G	V	Q	E	Y	V	E	F	K	I	N	I	P	377
AGA	AGG	CTG	TCT	GAG	GAT	TTA	GGA	GTT	CAA	GAA	TAT	GTG	GAA	TTT	AAA	ATA	AAC	ATT	CCA	1131
F	D	E	L	K	N	Y	L	S	E	A	T	I	G	L	H	T	M	W	N	397
TTT	GAT	GAA	TTA	AAG	AAT	TAT	TTG	TCT	GAA	GCA	ACA	ATT	GGT	CTG	CAT	ACC	ATG	TGG	AAC	1191
E	H	F	G	I	G	V	V	E	C	M	A	A	G	T	I	I	L	A	H	417
GAG	CAT	TTT	GGG	ATT	GGA	GTT	GTG	GAG	TGT	ATG	GCA	GCT	GGC	ACA	ATT	ATC	CTT	GCA	CAC	1251
N	S	G	G	P	K	L	D	I	V	P	V	H	E	G	D	I	T	G	F	437
AAT	TCG	GGG	GGC	CCA	AAG	CTT	GAC	ATT	GTG	GTT	CCT	CAC	GAA	GGA	GAT	ATA	ACT	GGC	TTT	1311
L	A	E	S	E	E	D	Y	A	E	T	I	A	H	I	L	S	M	S	A	457
CTG	GCT	GAG	AGT	GAA	GAA	GAC	TAT	GCT	GAA	ACT	ATC	GCT	CAC	ATT	CTT	TCC	ATG	TCT	GCA	1371
E	K	R	L	Q	I	R	K	S	A	R	A	S	V	S	R	F	S	D	Q	477
GAA	AAG	AGA	CTC	CAA	ATC	AGA	AAA	AGT	GCT	CGT	GCA	TCT	GTA	AGC	AGA	TTC	TCT	GAT	CAG	1431
E	F	E	V	T	F	L	S	S	V	E	K	L	F	K	*					492
GAA	TTT	GAA	GTG	ACA	TTC	CTA	TCA	TCT	GTG	GAA	AAG	TTA	TTT	AAG	TAA					1479

TGCCATATCTGTAAAATTAAAGATATTTTATATAAACTGGTTAAACACCTTCATATGTAAATATTTTCTAAATTCAAT
 CTCATTTGTCAAATCATTTTACTTTAGAAAAACAGACAAAATTTCCCTTTAGAAATAAAGGAAGTGTGAAAAGAAAATG
 GATGACTAGCCTTCGGCTTCCATTCTTGGTATACATGAGAGAGGCTGGCTGCTGAGATGAATGTGAACCAGGTTGCAGA
 GAATCTGGCTTTGAGGCCACCAGGAAGAACTAGTGGATTTGCCAAAAAACTACCCCTTGAGTGAAAATGAAGATGAGGGG

Fig. 3C

GACAGTGATGGAGAGAAAGCATCAAAGCTTCTGGAAGCAATCATTTCCCTTGATGGAAAGAAATAGCGGAAATTGG
CTGAGAGGTCTGAGGCTAGTCTGAAAGTGTACAGTTCAGTGTCTGAAGGATCAGGAGAAAAGCTGGGCCCTTGC
AGATCTGCTTGAGCCCGTTAAACTTCATCTTCTTGGCCACTGTAAAAAGCAACTGAATAGAGTCAAAATCAAAGAAG
GTGGTGAGTTACCTCTTAACAAAAGAAAAAATTGAACAGATCCACAGAGAAAGTAGCATTCAGTAAAACTTCACAGGTCC
TCTCCAAATGGGACCCCTATCATCTGAAGAACAGCAGCAGCAGCTGGTTTTCCTCCCTGGGGAAGGAGCCAGC
CATTGCTCCCATTGAACATGCGCTCAGTGGCTGGAAGGCAAGAACTCCCTGGAGCAGGAAATTTTAACTCCTCCAT
AAGAACAAAGCAGCAGTGACAGATCCTTACTGACTCCCATGGAAAAGGCCCTCTCTCCAAGCCATGAGCCTGGAAGAGG
CAAAGATGCACCGAGCAGAGCTTCAGAGGGCTCGGGCTCTGCAGTCTACTATGAGGCCAAGGCTCGAAAAGAGAAAGAA
AATCAAAAGTAAAGATATCACAAAGTCGTGAAGAAAGGAAAGCCCTTAAAGAGTTTGAGCAGCTACAG
AAGGTTAATCCAACTGTGGCACTGGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

Fig. 3D

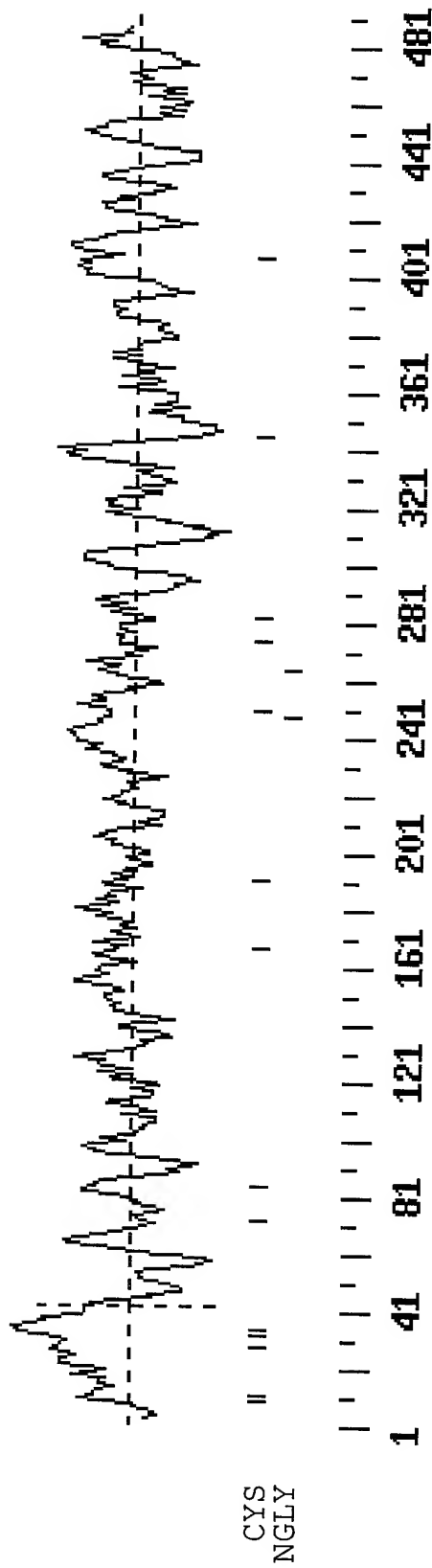


Fig. 4

Fig. 5A

Fig. 5B

Fig. 5C

MUS_GT1	PVTMLKCHHLKGNQL	WEYDPVKLTLOHVNS	NQCLDKATEEDSQVP	SIRDCSGRSQQWLL
RAT_GT1	PVTMLKCHHLKGNQL	WEYDPVKLTLOHVNS	NQCLDKATEEDSQVP	SIRDCSGRSQQWLL
HUM_GT1	PVTMLKCHHLKGNQL	WEYDPVKLTLOHVNS	NQCLDKATEEDSQVP	SIRDCSGRSQQWLL
COW_GT1	PVTMLKCHHLKGNQL	WEYDPVKLTLOHVNS	NQCLDKATEEDSQVP	SIRDCSGRSQQWLL
PIG_GT1	PVTMLKCHHLKGNQL	WEYDPVKLTLOHVNS	NQCLDKATEEDSQVP	SIRDCSGRSQQWLL
47169	PVTLYDCHSMKGNQL	WKYR-KDKTLYHPVS	GSCMDCS-ESDHRIF	MNTCNPSSLTQQWLF

MUS_GT1 R--NVTLP E I F-----
RAT_GT1 R--NVTLP E I F-----
HUM_GT1 R--NVTLP E I F-----
COW_GT1 R--NVTLP E I F-----
PIG_GT1 R--NVTLP E I F-----
47169 EHTNSTVLEKFN RN
. ; : : :

Fig. 5D

gly-5b	----	MIIFKKKAILK	VLLVPVFWICSLIF	FAATSNDS	SSQIGSNN	DLANK--	IAEANFHP							
gly-6a	--MIASLIR	RRRRSR	RCVVYSV	FLFGFLAL	WGSFALAL	VFLSDMY	IGEDQ--	ISTQKA	IK					
gly-3	--MLS	VGGRS	AVCR	AVIATSIV	WLLIDVV	ILFY	YLDP	STSQQP	FPEDNR	ILNRAR	RIE			
gly-4	-----	MLPRML	KMKT	VGTVIA	VIWFLGLAF	IYVQ	STSS	SLRPPGR	HPPPLP	--QLDPL	IP			
gly-9	-----	MLRYII	IPRKK	GTFVIA	AFLTVAFFC	IVAY	HRNDR	RRRTKFKQ	FPDIEK	YAEEL	VLRLP			
47169	-----	MRRKE	KRLI	Q	VALVLA	ALLLPN	VGLW	ALYRER	QPDGT	PGSG	AAVAPAA	GQG		
gly-5b	KAAKQD	VIQFG	PPPI	EPEPV	VENNK	VEEEE	QPGGN	LAKPK	FMVDP	NDPI	YKKG	DAQA	AGE	
gly-6a	PIARSN	YHV	VVGHYN	GNLPED	KKRNL	TSEE	LNAN	-----	LYAP	HD	-----	---	DWGE	
gly-3	PLPPAA	QHDSD	PDPAH	PIQPEK	QEKQ	VYPVD	KETAN	QLRKL	METQA	FGPG	-----	---	YHGQ	
gly-4	QNPPQN	DEIR	PKKA	PIPTIN	LAED	TTIH	ERTEK	D---	VT---	--	-----	---	WKT	
gly-9	ETWNGE	LHQI	PNYTA	PR--	EGP	----	----	-----	---	----	-----	---	GE	
47169	SHSRQ	KKTF	FLGDGQ	KLKD	WHDKE	AIRRDA	Q	RVGN	-----	---	-----	---	GE	
gly-5b	IGKAVV	VDKTK	LSTE	EKAKY	DKGML	NNAFN	QYAS	DMI	SVHRTLPT	NIDA	ECKT	---	EKYN	
gly-6a	GG--	AGVS	--HLTPE	QQKLAD	STFAV	NQFN	LLVSD	GISV	RRSLPE	IRKP	SCRN	---	MTYP	
gly-3	GGTG	VTP	-----	ED	KKTIKE	KRFL	ENQFN	VVASE	MISV	NRTL	LPD	YRSD	ACRTSGNN	LKT
gly-4	FDVEK	FLN	-----	KG	KWHQ	GEDK	YKAN	SFN	QEAS	DALN	PTRKIPD	SREP	QCRD	--VDYSK
gly-9	KGKP	VVL	TG-----	K	DAELG	QADM	KKWF	EMN	VHAS	DKISL	DRDVPD	PRIO	ACKD	--IKYDY
47169	QGRPY	PMT	-----	DAER	VDQ	AYRE	NGFN	IYVSD	KISL	NRSLPD	IRHP	CNCS	---	KRYL

Fig. 6A

g1y-5b	ENLPRTSVIICFHNE	AWSVLLRRTVHSVLER	TPDHLLLEEVLVDDF	SDMDHTKRP-LEEYN
g1y-6a	DNLPTTSVIIYHNE	AYSTLLRRTVWSVIDR	SPKELLKEIILVDDF	SDREFLRYPTLDTTL
g1y-3	AGMPKTSIIIVFHNE	AWTTLRLTLHSVINR	SPRHLLLEEIILVDDK	SDRDYLVKP-LDSYI
g1y-4	VGMQPTTVIITYHNE	ARSSLLRRTVFSVFNQ	SPEELLLEIIVLDDN	SQDVEIGKE-L----
g1y-9	AALPKTSVIIIFTDE	AWTPLLRTVHSVINR	SPPELLQEVILLDDN	SKRQELQEP-LDEHI
47169	ETLPNTSIIIPFHNE	GWSSLLRRTVHSVILNR	SPPELVAEIIVLDDF	SDREHLKKP-LEDY-
	:::~::~:	:::~::~:	:::~::~:	:::~::~:
g1y-5b	--SQFGGKVILRME	KREGLIRARLRGAAV	ATGEVLTYLDSHCEC	MEGWMEPLLDRIKRD
g1y-6a	--KPLPTDIKIIRSK	ERVGLIRARMMGAQE	AQGDVLTFLDSHCEC	TKGWLEPLLTRIKLN
g1y-3	--KMFFPIPIHLVHLE	NRSGLLIRARLTGSEM	AKGKILLFLDAHVEV	TDGWLEPLVSRVAED
g1y-4	---AQIQRITVLRNN	QREGLIRSRVKGAQV	ARAPVLTFLDSHIEC	NQKWLEPLLARIAEN
g1y-9	--KRFGGKVRLIRKH	DRHGLIRAKLAGARE	AVGDIIVFLDSHCEA	NHGWLEPIVQRI SDE
47169	--MALFPSVRILRTK	KREGLIRTRMLGASV	ATGDVITFLDSHCEA	NVNWLPPLLDRIARN
	::::: .	:::~::~:	:::~::~:	:::~::~:
g1y-5b	PTTVVCPVIDVIDDN	TFEYHHSKAYFTSV-	-GGFDWGLQFNWHSI	P-ERDRKNRTRPIDP
g1y-6a	RKAVPCCPVIDIINDN	TFQYQKGIEMFR---	-GGFNWNLQFRWYGM	PTAMAKQHLLDPTGP
g1y-3	RKRVVAPIIDVISDD	TFEYVTASETTWG--	--GFNWHILNFRWYAV	PKRELNRRCGSDRSMP
g1y-4	PKAVVAPIIDVINVD	NFNYPVGASADLR---	-GGFDWTLVFRWEFM	NEQLRKERHAHPTAP
g1y-9	RTAIVCPMIDSISDN	TLAYHGDWSLST---	-GGFSWALHFTWEGL	S-EEEQKRRTKPTDY
47169	RKTIVCPMIDVIDHD	DFRYETQAGDAMR--	-GAFDWEMYKRIPI	P---PELQKADPSDP
	:::::~::~:	:::~::~:	:::~::~:	:::~::~:

Fig. 6B

Fig. 6C

gly-5b	QCHGQGGN-----Q	YWMLSKDGEIRRDE-	-----SCVDYAGS	DVMVFPCHGMKGNQE
gly-6a	CLKIFHKT-----Q	LWLYTGDRRIRTEH	-LCLSVVQLLHTTSD	WKIQLKECAGFDTEY
gly-3	ACHGAGGN-----Q	AWSLTGKGEIRSDDL	-CLSSGHVYQIGSEL	KLERCSVSKINVKHV
gly-4	GCHGTGGN-----Q	EWVFDQLTKTFKNAI	-----SQLCLDFSSN	TENKTVTMVKCENLR
gly-9	HCQKGSSP-----Q	LMSLSKEGNLRREN-	-----TCASEEN	GNIRMKTCSSKKAQFN
47169	GCVRGRGEAAWNNMQ	VFTEFWREDIRPGDP	QHTKKFCFDAISHTS	PVTLYDCHSMKGNQL
	:	:	:	:

gly-5b	WRYNHDTGRLQHVS	QKCLG-----MTK	DGAKLEMVACQYDDP	YQHWKFEYNEAKAI
gly-6a	WDFKPKIGRFQNRKT	GLCLASPDIFDPTKD	EFNPPIVQKCRSSND	RQNWITITEMSWLPEH
gly-3	FVFDDQAGTLLHKKT	GKCVTG-----AD	QRTLDECGLGRKD-	-QMWOLEGYQSP---
gly-4	PDTMVVEKNGWLTQG	GKCLTVNQG-----SG	GDWLIYGAHCELNNG	AQRWIFEKLDITYE--
gly-9	ERWAYENKMIRNLKS	GKCMSTAN-----LK	PGDNAIVVECDEKDE	HQKWNFIDPAKA---
47169	WKYRKDK-TLYHPVS	GSCMDCS-----ES	DHRIFMNTCNPSSLT	-QQWLFETHNSTVLE

gly-5b	EHGAKPPS			
gly-6a	P-----			
gly-3	-----			
gly-4	-----			
gly-9	-----			
47169	KFNRN---			

Fig. 6D